

Pred. No.:	Score:	Length:
	665.00	5450
	100.0%	665
	100.0%	0
Query Match:	100.0%	Mismatches:
DB:	6	Indels:
		Gaps:
US-10-029-345A-109	(1-665) x AX482439	(1-5450)
Qy	1 MetalahisGluMetIleGlyThrGlnileValThrGluArgLeuValAlaLeuLeuGlu	20
Db	538 ATGGCCCATAGCATATGATTGAACTCTCAATGTGAACTTCATACATATCC	597
Qy	21 SerGlyThrGluGlyValLeuLeuLeuAspSerAspProValGluTyRasnTrSer	40
Db	598 AGTGGACGGAAGAAGTGCTGTTAATGATAGCCGCATTTGGSATACTATATCC	657
Qy	41 HistLeuLeuGluAlaLeuAsnLeuAsnLeuAsnCysSerLysLeuMetLysAargLeuGlnGln	60
Db	658 CACATTGAGGCCATTAATACATGCTGTCACACTATGAGCGAACGTTGACAG	717
Qy	61 AspLeuValLeuThrGluLeuIleGlnHisSerAlaLysValAspIleAsp	80
Db	718 GACAAGTGTATTAGCTGAGCTCATCCAGTCGCGAACATAGGTGACATGAT	777
Qy	81 CysSerGlnIlyValValValTyRapGlnSerSerGlnIlyValAlaSerLeuSerSer	100
Db	778 TGCAGCTGAGAAGGTCTAGTTAGCTCAAGCTCCAGTGTCTCTCTCTCA	837
Qy	101 ASPcSPhelLeuThrValLeuLeuGlyLysLeuGluLysSerPhelSerValHisLeu	120
Db	838 GACTGTTCCTCACTCTACTCTGCTGTTAATCTGCTGTTCTGCTGCTG 897	957
Qy	121 LeuIaGlyGlyPheIaGluPheSerArgcysPheProGlyLeuGlyLysSer	140
Db	898 CTGGCAGGIGGTTCTGACTCTGCTCTGTTCTGCTGCTGCTG 957	1918
Qy	141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaLeuIleGlyProThr	160
Db	958 ACTCTAGTCCTACCGCATTTCTCGCACATGCGCAACC 1017	2038
Qy	161 ArgLeuLeuProAsnLeuThrLeuGlyLysGlnGlyGlyAspValLeuAsnIlyGluLeuIle	180
Db	1018 CGAATCTCTCCAACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077	2098
Qy	181 GluGlnIaGlyGlyIleGlyTyRValLeuAsnAlaSerTyRThrCysProSphe	200
Db	1078 CAGCAGATGGATGGATGTTATGTTAATGCCAGTAACTCTGCTGCTGCTGCTG 1137	2158
Qy	201 IleProGluSerHisPheLeuArgcysProValAsnAspSerPhcysGluIleIleu	220
Db	1138 ATCCCCGAGCTCATCTCCGCGGCGCTGTGAGACGCTTGTGAGAAATTGCG 1197	2218
Qy	221 ProTproLeuAspSerValAspPhelIleGluIlyAlaIlyAlaSerGlnGlyIlyVal	240
Db	1198 CGGTTGGTGGACAAATCTAGATTCATTGAGAGCAAAAGCTCCATGGATGTT	1257
Qy	241 LeuValHisIleGlyLeuAspSerArgcysSerAlaThrIleAlaIleAlaIleTyRileMet	260
Db	1258 CTGAGCAGCTGTTAGCTGGATCTCCGGTCCGCCCCATCGCTACATCAG 1317	561
Qy	261 LysArgMetAspMetSerIeAspGlnIaTyRArgPhenValIleGluSerAspPro	280
Db	1318 AAGAGGATGGACATGCTTGTAGCTACAGTTGTGAGAAAGACCTACT 1377	2278
Qy	281 IleSerProAsnProAsnIleGlyGlyLeuLeuAspTyRgulYIlyValGlyAsn	300
Db	1378 ATATCTCCAACTTCATTTCTGGCCACTCTGCTGACTATGAGAGGAGTAAAC 1437	601 GluIlyProSerAspArgAlaAspSerArgcysSerGlnValTySerValArgArg
Qy	301 GluIlyProSerAspArgcysSerIleLeuLeuIleGluGlyProAsnProAsn	320
Db	1438 CAGACTGGAGCATCAGGSCCAAGAGCAACTCAGCTGCACTGGAGAGCCAACT 1497	661 IleIleGluValSer
Qy		665
Db		2518 ATCATGAGTCCT 2532

Db 1918 GATAGGAGGAGGCAGCATCCCCAGAACAGCTTCAAGACAGCCAG 1977
 Qy 481 SerIysArgLeuHisSerValArgThrSerSerSerGlySerGlyThralAglLargSerLeuLeu 500
 Db 1978 AGCAGGATTCATTCGCTTCAGACAGCAAGTGCCACCCAGGGCTTA 2037
 Qy 501 SerProLeuHisArgSerGlySerValGluAspAspSerTyrHisthrSerPheLeuPheLeuPhcIY 520
 Db 2038 TCTCACCTGCTCGAGGGGGCTGGAGCACTACACACAGCTTCTTCGCC 2097
 Qy 521 LeuSerThrSerGlnGlnLisLeuThrLysSerAlaGlyLeuIleLysGlyTyrHis 540
 Db 2098 CTTTCCACCCAGCCAGCAGCCTCTACAGGATCTCTGACCTGGCCCTTAAGGCTGGCAC 2157
 Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560
 Db 2158 TCGGATATCCTGGCCCCAGACCTCTACCCCTTCCCTGACAGCAGCAGCTGGATTTGCC 2217
 Qy 561 ThrCluSerSerHisPheTyrSerAlaSerAlaLeuTyrglyIysSerAlaSerTyrSer 580
 Db 2218 ACAGAGTCCTCACTCTACTCTGCCCAGGCACTACGGGACTGGCCAGTACTCT 2277
 Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 600
 Db 2278 GCCTACAGCTGCAACGCTGCCACTCTGCGAGACCAGCTATTCTGIGGCAGGGGG 2337
 Qy 601 GluIysProSerAspAspGlyAlaAspSerArgArgSerTyrPheIgluUserProPheGlu 620
 Db 2338 CAGAGGCCAGTGAAGCTGCACTCGCGCGAGCTGCGATGAGAGAGCCCTTGAA 2397
 Qy 621 IysGlnPheLysArgArgSerCysGlyMetGluPheGlyGluUserIleMetSerGluAsn 640
 Db 2398 AACGAGTTAAACGAGCTGCCAAATGGAATTGAGACAGCATCATGAGAAC 2457
 Qy 641 ArgSerArgGluGluLeuGlyIysValGlySerGlnSerSerPheSerGlySerMetGlu 660
 Db 2458 AGTCACCGGAAAGCTGGGAAGTGGGAGCTGAGCTAGCTTGGGGCATGGAA 2517
 Qy 661 IleIleGluValSer 665
 Db 2518 ATCATTGGGTCTCC 2532

Search completed: June 24, 2004, 01:46:29
 Job time : 6003 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: June 23, 2004, 19:31:01 ; Search time 615 Seconds
(without alignments)

4533.580 Million cell updates/sec
Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 MAHEMIGQIVTERLVALLE.....LGKVGSQSFSGSMEIEVS 665

Scoring table: OLIGO
Xgapop 60.0 Xgapext 60.0
Igapop 60.0 Igapext 60.0
Fgapop 6.0 Fgapext 7.0
Delop 6.0 Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 473

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODE=frame+_p2n.model -DBV=x1P
-DB=N_GeneSeq_29Jan04_QFMP=FastaP -SUFFIX=012.FNG -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=75 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=473 -ALIGN=50 -MODE=LOCAL
-OUTFILE=pto -NORM=ext -HEPSIZE=500 -MINLEN=200000000 -MAXLEN=200000000
-USERUS10029345 @CGN 1 1 708 @runat 23052004 121751 25585 -NCPU=6 -ICPU=3
-NO MAP -LARGEHEADER -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBU TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=60 -XGAPEXT=60 -FGAPDP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=7 -DBLOP=6 -DBLEXT=7

Database : N_GeneSeq_29Jan04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	665	100.0	5450 6 ACC0559	Acc60559 Polynucle
2	665	100.0	5450 6 ACC60572	Acc60572 Polynucle

ALIGNMENTS

RESULT 1
ACCC60559

ID ACC60559 standard; cDNA; 5450 BP.

XX ACC60559;

AC ACC60559;

XX 19-JUN-2003 (first entry)

DE Polynucleotide relating to the invention SEQ ID NO: 108.

XK Gene; BS; antiproliferative; hepatotropic; nephrotropic; antiarthritic; KW antiisorotic; cardiant; cytotoxic; gene therapy; liver disease; KW proliferative disorder; renal failure; cardiovascular disorder; KW immunological disorder; arthritis; psoriasis; congenital heart defect; KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.

XK OS Homo sapiens.

OS WO200257460-A2.

XX PDD

XX 25-JUL-2002.

XX PR 20-DEC-2001; 2001WO-US050459.

XX PR 20-DEC-2000; 2000US-0255668P.

XX PR 30-MAR-2001; 2001US-0287735P.

XX PR 05-JUN-2001; 2001US-0295448P.

XX PR 25-JUN-2001; 2001US-0300465P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L; PI Siemers N, Bol D, Schiaven G, Finger J, Toddrud CG, Bassolino D;

PI PI Krystek S, McAtee P, Suchard S, Banas D;

XX DR DR P-P5DB; ABR52381.

XX PT WPI: 2002-599721/64.

XX PT Novel polynucleotides encoding human phosphatase polypeptides useful in the prevention or treatment of e.g. proliferative and cardiovascular disorders.

XX PS Claim 1, Fig 13; 801PP; English.

The invention relates to a novel isolated nucleic acid comprising a polynucleotide having a nucleotide sequence selected from 40 polyribonucleotides fully defined in the specification. The polynucleotide of the invention has antiproliferative, hepatotropic, nephrotropic, antiarthritic, antiparotic, cardiant, and cytotoxic activity. The polynucleotide may have a use in gene therapy. A polynucleotide or polypeptide of the invention is useful for preventing, treating or ameliorating a medical condition, e.g. a proliferative disorder. They are also useful for treating e.g. liver disease, renal failure, immunological disorders including arthritis and psoriasis, cardiovascular disorders such as congenital heart defect and congestive heart failure, and cancer. A method of the invention is useful for diagnosing a pathological condition or susceptibility to a condition in a subject. The present sequence is used in the exemplification of the invention

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

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XX Score: 665.00

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XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

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XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

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XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

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XX Best Local Similarity: 100.00%

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XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

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XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

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XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 6

XX Gap:

XX Length: 5450

XX Matches: 665

XX Conservative: 0

XX Mismatches: 0

XX Indels: 0

XX Gap: 0

XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;

XX SQ Alignment Scores:

XX Pred. No.: 0

XX Score: 665.00

XX Percent Similarity: 100.00%

</div

KW immunological disorder; arthritis; psoriasis; congenital heart defect; congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX
OS
XX Homo sapiens.
PN WO200257460-A2.
PD 25-JUL-2002.
PP 20-DEC-2001; 2001WO-US050459.
XX
PR 20-DEC-2000; 2000US-025686P.
XX MAR-2001; 2001US-0280186P.
PR 01-MAY-2001; 2001US-0287735P.
PR 05-JUN-2001; 2001US-0295848P.
XX 25-JUN-2001; 2001US-0300465P.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L; Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
PI Kryteck S, Mcatee P, Suchard S, Banas D;
XX
DR WPI; 2002-599721/64.
DR P-PSDB; ABRS2407.
XX
PT Novel polynucleotides encoding human phosphatase polypeptides useful in the prevention or treatment of e.g. proliferative and cardiovascular disorders.
XX
PS Example 7; Fig 19; 801pp; English.
XX
CC The invention relates to a novel isolated nucleic acid comprising a polynucleotide having a nucleotide sequence selected from 40 polymonucleotides fully defined in the specification. The polynucleotide of the invention has antiproliferative, hepatotropic, nephrotropic, antiarthritic, antipsoriatic, cardiotropic, and cytotropic activity. The
CC polynucleotide may have a use in gene therapy. A polynucleotide or polypeptide of the invention is useful for preventing, treating or ameliorating a medical condition, e.g., a proliferative disorder. They are also useful for treating e.g. liver disease, renal failure, immunological disorders including arthritis and psoriasis, cardiovascular disorders such as congenital heart defects and congestive heart failure, and cancer. A method of the invention is useful for diagnosing a pathological condition or susceptibility to a condition in a subject. The present sequence is used in the exemplification of the invention
CC Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 0 **Length:** 5450
Score: 665.00 **Matches:** 665 **Conservative:** 0
Percent Similarity: 100.0% **Mismatches:** 0
Best Local Similarity: 100.0%
Query Match: 6 **Indels:** 0
DB: Gaps: 0
US-10-029-345A-109 (1-665) x ACC60572 (1-5450)
QV 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 538 ATGCCCTGAGATGATGAACTCAATGTTACTGAGGGTGGAGCTCTGGAA 597
QV 21 SerGlyTyrGluLysValLeuLeuLeuSerProValSerAlaGluGlyTyrSerAsp 40
Db 598 AGTCGAACGGAAAGTGCTGTATTGATAGCGGCATTGGAAATACAATCACCC 657
QV 41 HisIleLeuGluAlaLeuAsnAsnCysSerLeuMetLysArgLeuGlnGln 60
Db 658 CACATTGGAACCTTAATCACTGCTCAAGCTTAGAGGAGGTTGCAACAG 717
QV 61 AspGlyValLeuIleThrGluLeuIleGlnHisSerAlaLysLysLysValAsp 80
Db 718 GACAAGGTAAATTACAGAGCTCATCGACATTCGGCAACATAAGTTGACATGT 777
QV 81 CysSerGlnLysValValValThrAspGlnSerSerGlnSerGlnValAlaSerSer 100
Db 778 TGCAGTCAGAACGGTGTGACTTTACGATCAAGCTCCAGATGTCGCCCTCTCTCTCA 837
QV 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
Db 838 GACGTGTTCTACTGACTTCGGTAACCTGGAGAGAGCTTCACCTGTTGACCTG 897
QV 121 LeuValGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 898 CTTCAGGGGGTTGCTGAGGTTCTGTTCTGTTCTGTTCTGGCCCTCTGTTAGGAAATCC 957
QV 141 ThreLeuValProThrCysLeuSerGlnProValAlaAsnLeuGlyProThr 160
Db 958 ACTCTAGRCCTACCTGCTTCACTGCTTCAAGCTTGTGTTCCACATGGGCCAAC 1017
QV 161 ArgLeuProAsnLeuThrValLeuGlyCysGlnGargAspValLeuAsnLysGluLeuIle 180
Db 1018 CGAACTCTCCAACTTATCTGGCTCCGGAGATGCTTCAAGAGGACTGATA 1077
QV 181 GluGlnAsnGlyLysLeuGlyLysValLeuAsnLeuSerThrCysProLeuAsp 200
Db 1078 CAGGAGAACTGGATGTTGTTATGCTTAAATGCCGCTATACTCTCCACAGGCTGACTT 1137
QV 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluValLeu 220
Db 1138 ATCCCCGAGTCATTCCTCCGCGTGCCTGATGACAGCTTGTGAGAAATTG 1197
QV 221 ProTrpLeuAspLysSerValAspPheThreGluLysAlaSerArgSerVal 240
Db 1198 CCGTGGTGGACAACTACTAGATGATTCATGAGAAAGCCTCCATGGATG 1257
QV 241 LeuValHisCysLeuValGlyLysSerArgSerAlaThrLeuAlaLeuAlaTyrosine 260
Db 1318 AGAGGATGAGCAGTCCTTGTAGATGAGCTTACGATTTGAGAGAAAACCTACT 1377
Db 1258 CTATGCACTGTTAGCTGGATCTCCGCTCCGCCACCATGCTTACATG 1317
QV 261 LysArgMetAspMetSerLeuAspGluIaLysArgPheValLysGluLysArgProThr 280
Db 1318 AGAGGATGAGCAGTCCTTGTAGATGAGCTTACGATTTGAGAGAAAACCTACT 1377
QV 281 IleSerProAsnPheAsnPheAsnLeuGlyGlnLeuLeuAspProThrGluLysSerIleLysAsn 300
Db 1378 ATATCCTCAATCTCAATTCTGGCCACTCTGGACTATGAGAGAGATAGAAC 1437
QV 301 GluThrGlyAlaSerGlyProLysSerIleLeuLeuLysLeuLysLeuLysProAsn 320
Db 1438 CAGACTGAGCATCAGGCCAAAGGAAACTCAAGCTCTGCACCTGAGGACCAAT 1497
QV 321 GluProValProAlaValSerGluGlyGlyLysSerGluThrProLeuSerPro 340
Db 1498 GAACCTGCCCCGCTGCTCAGGGTGGACAGAAAGGGACGCCCTCTGTCACCC 1557
QV 341 CysAlaAspSerAlaLysSerGluAlaLysLysGlnArgProValHisProAlaSerVal 360
Db 1558 TGTCGCGACTCTGCTACCTGAGGAGCAGGACAAGGCCCGTCATCCGGCAGGCC 1617
QV 361 ProSerValProSerValGlnProSerLeuLeuGluAspProLeuValGlnAlaLeu 380
Db 1618 CCCAGCGGCCAACGCTGAGCGCTGCGCTGAGGACGCCGCTGCTAACGGCTC 1677
QV 381 SerGlyLeuLysLeuSerAlaAspPheLeuGluAspSerAsnIleLeuLysArgSerPhe 400
Db 1678 AGTGGCTCACCTGTCGCCAGACGGCTGGAGCAAGCTAACATGCTCAGGGCTCTC 1737
QV 401 SerLeuAspLeuSerValSerValSerAlaSerMetAlaLysSerLeuIleGlyPhe 420
Db 1738 TCTCTGAGATCAATCACTTCACTGAGCTGAGCTGAGCTTCACTGCTC 1797
QV 421 SerSerSerGlyLysPheLeuGlyGlyProSerThrThrLeuAspGlyThreon 440
Db 1798 TTCTCATGAGAATGCTGTGAGTACTACAACCTCTCACTGATGAGGACCAAC 1857

Qy 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGlnLysThrProGluThrSerPro 460
 Db 1858 AACGTTATGCCAGTCRCCCTGTCAAGAACTATGGAGCGACGCCAACAGTCCT 1917
 Qy 461 AspLysGluGluAlaSerIleProLysLeuGlnThrAlaArgProAspSerGln 480
 Db 1918 GATAAGGAGGAGGCCAGCAGCAGCCAGAAGACTGAGACGCCACGCCCTTGAGGCCAG 1977
 Qy 481 SerLysArgLeuHiSerValArgThrSerSerSerGlyLysThrAlaGlnArgSerLeu 500
 Db 1978 AGCAAGGATGATGCGTGGAGCCAGCAGCAGTGAGCAGCCAGGCTTGAGGCCAG 2037
 Qy 501 SerProLeuHiArgSerGlySerValGluAspAsnTYHiSerSerSerLeuPheGly 520
 Db 2038 TCTTCACTGCTGATCGAGTGGAGGAGCTGGAGCAATTACCAACAGCTTCCTTTGAG 2097
 Qy 521 IeuSerThrSerGlnLysIleThrLysSerAlaGlyLeuLysGlyTyros 540
 Db 2098 CTTTCCACCAAGCCAGCAGCACTTACAGAAGCTGCTGCCTAGGCTTGAGCTGGAC 2157
 Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpTyPheAla 560
 Db 2158 TCGGAATATCGGCCCGACGCTTACCCCTTACCCCTTGACCCAGCTGGTTTGGCC 2217
 Qy 561 ThrGluSerSerHisPheTyrSerAlaSerAlaLeuTyrGlyGlySerAlaSerTyrSer 580
 Db 2218 ACAGAGTCTCACACTCTACTCTCTCCCTCAGCCATCTAGGAGGAGCTGGCCAGTACTCT 2277
 Qy 581 AlaTyrSerGlySerGlnIeuProThrCysGlyAspGlnValThrSerValArgArg 600
 Db 2278 GCCTTACAGCTGAGCCAGCTGCCACTTGCGGAGACCTATTCCTGTCGCGCAGGG 2337
 Qy 601 GlutlysProSerPAPGalaAspSerArgSerTPhiGluGluSerProPheGlu 620
 Db 2338 CAGAGGCCIAAGTGACAGACTGACTCGGGGGAGCTGCGCATGAGAGGCCCTTGAA 2397
 Qy 621 LysGlnPheLysSerGargSerCysGlnMetGluPheGlyGluSerIleMetSerGluasn 640
 Db 2398 AAGAGCTTAACCCAGAGCTGCCAATGGAAATTGGAGGAGCATATGTCAGAGAAC 2457
 Qy 641 ArgSerArgGluGluLeuLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
 Db 2458 AGGTCACGGAGAGCTGGGAAGTGGCAAGTCAGTCAGTTTGGCAAGCATGGAA 2517
 Qy 661 IleLeuIvaIleSer 665
 Db 2518 ATCATTGAGGTCTCC 2532

Search completed: June 24, 2004, 00:04:41
 Job time : 624 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:

June 23, 2004; 23:00:42 ; Search time 3667 Seconds

(without alignments) 5415.421 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665

Sequence: 1 MAHEMIGQIVTVERLVALV.....LGKVGSQSFSGSMELIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27153289 seqs, 14931090276 residues

Word size:

473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODE=frame+pin.model -DEV=xlp
-O=/com2_1/usproto/spool/p/IS10029345/runat_23062004_121752_25604/app_query.fasta_1.839
-DB=OLIGO -QMT=fastap -SUFFIX=olig2.lst -MINMATCH=0.1 -LOOPCLD=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo.cdi -LIST=75
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=473 -ALIGN=50 -MODE=LOCAL
-OUTFILE=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USERINFO=US10029345 @CGN 1 15180 @runat_23062004_121752_25604 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DBLOP=6 -DELEXT=7

Database :

```

EST:*
1: em_estaba:*
2: em_estahum:*
3: em_estain:*
4: em_estam:*
5: em_estav:*
6: em_esapl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mub:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssi:*
```

29: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
SUMMARIES					

No matches found

Search completed: June 24, 2004, 02:47:42
Job time : 3667 secs

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No matches found
 Search completed: June 24, 2004, 03:01:36
 Job time : 666 secs

Title: US-10-029-345A-109
 Perfect score: 665
 Sequence: 1 MAHEMIGQIVIERRVALLER.....LGKVGQSOSFSGSMEIEVS 665
 (without alignment)
 4574.211 Million cell updates/sec

Scoring table: OLIGO
 Xgpop 60.0 Xgapext 60.0
 Igpop 60.0 Igapext 60.0
 Fgpop 6.0 Fgapext 7.0
 Delop 6.0 Delext 7.0

Searched: 3017426 seqs, 229054650 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
 -MODEL=frame+pn.model -DEV=xip
 -Q=/cgn2_1/us/proj/spool_p/1US10029345/runat_23062004_121753_25636/app_query.fasta_1.839
 -DBs=Published_Applications_NA_QPMfile12.rnpb -MINMatch=0.1
 -LOOP=0 -LOOPEXT=0 -UNITS=bigs -START=1 -END=1 -MATRIX=oligo
 -TRANS=human40_cdi -LIST=5 -DOALIGN=200 -THR SCORE=quality -THR MIN=473
 -ALIGN=50 -MODEL=LOCAL -OUTFMT_PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0
 -MAXLEN=200000000 -USER=@CGN_1.1_723 @runat_23062004_121753_25636
 -NCPU=6 -CPU=3 -NO MMAP -LARGESQRTY -NEG SCORES=0 -WAIT -DBBLOCK=100
 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=60 -XGAPEXT=60
 -DBLOP=6 -FGAPDP=60 -FGAPEXT=7 -YGAPDP=60 -YGAPEXT=60 -DBLEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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On protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:25:13 ; Search time 139 seconds
(without alignments)

Title: US-10-029-345A-109
Perfect score: 665

Sequence: 1 MAHEMIGQIVIIRRVALLE.....LGKVGQSOSFSGSMEIEVS 665
2654.981 Million cell updates/sec

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Igapop 60.0 , Igapext 60.0
Fgapop 6.0 , Fgapext 7.0
DelOp 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xip
-Q=/cgn2_1/usproc/spool/p1us10029345/runat_23062004_121753_25617/app_query.fasta_1.819
-DB=Issued_Patents_NA_QFMTfaftcap -SUFFIX=_012.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=512 -START=1 -END=1 -MATRIX=XoOl1go -TRANS=human40_cdi
-LIST=75 -DOALIGN=200 -THR SCORE=quality -THR MIN=473 -ALIGN=50 -MOB=LOCAL
-OUTFILE=pto -NORMEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USERUS10029345 @CGN 1 1 105 @runat_23062004_121753_25617 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOp=60 -YGAPEXT=60 -DELOp=6 -DELExt=7

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCMS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
-	-	-	-	-

No matches found

Search completed: June 24, 2004, 02:50:16
Job time : 139 secs

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